

### **Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

#### **Listing of Claims**

1. (Currently amended) A method for analyzing a heterogeneous sample comprising a mixture of proteins, peptides, protein fragments or peptide fragments, the method comprising:
  - (a) separating the heterogeneous sample of proteins, peptides, protein fragments or peptide fragments, into classes by binding the members of each class to a antibodies or antigen binding fragments of antibodies thereof, each antibody, or fragment thereof specifically binding to a single motif that is present in greater than 2 different types of proteins, peptides, protein fragment or peptide fragment, each antibody or fragment thereof being fixed to spaced apart defined locations on an array, wherein more than one protein, peptide, protein fragment or peptide fragment binds to each defined location on the array, and wherein those proteins, peptides, or protein fragments or peptide fragments binding to a specific antibody or fragment thereof represent a class, the members of each class a motif common to that class; and
  - (b) characterizing by utilizing mass spectrometry, all the proteins, peptides, protein fragments or peptide fragments in each class by determining the mass of the proteins, peptides, protein fragments or peptide fragments in each of the classes, and determining the abundance of proteins, peptides, protein fragments or peptide fragments, of different mass in each of the classes, and wherein the characterization of the bound proteins, peptides, or protein fragments or peptide fragments occurs at the defined and discrete locations on the array.
2. (Previously presented) A method according to claim 1 wherein the heterogeneous sample of proteins, peptides, protein fragments or peptide fragments, is an extract of the total protein content of a cell or tissue type.
3. (Previously presented) A method according to claim 1 wherein, prior to performing step (a), there is a step of fragmenting the proteins and peptides in the heterogeneous sample to form protein fragments and peptide fragments.

4. (Previously presented) A method according to claim 3 wherein the step of fragmenting the heterogeneous sample is performed by chemical or enzymatic cleavage.
5. (Previously presented) A method according to claim 3 wherein the step of fragmenting the heterogeneous sample is performed using a sequence-directed cleavage mechanism.
6. (Previously presented) A method according to claim 3 wherein step of fragmenting the heterogeneous sample is performed by digestion of the heterogeneous sample of proteins or peptides with trypsin.
7. (Previously presented) A method according to claim 1 wherein the motif in each peptide, or protein or peptide fragment, is at the same location in each peptide, or protein or peptide fragment, relative to the C-terminus, the N-terminus, or an internal feature.
8. (Previously presented) A method according to claim 1 wherein the heterogeneous sample is a heterogeneous sample of protein fragments or peptide fragments and the motif in each fragment is at the same location in each fragment, relative to the site of cleavage.
9. (Previously presented) A method according to claim 1 wherein the motif in each peptide, or protein or peptide fragment, is three, four, five, six or more amino acids in length.
10. (Previously presented) A method according to claim 1 wherein the motif contains three, four or five variable amino acids, the other amino acids in the motif being constant between all peptides, or protein or peptide fragments.
11. (Previously presented) A method according claim 1 wherein the motif is at the C-terminus.
12. (Withdrawn) A method according to claim 1 wherein the motif is at the N-terminus.
13. (Previously presented) A method according to claim 1 wherein the array comprises a

number of different types of antibody, each type immobilized at a spaced apart defined location on the array, wherein each type of antibody is capable of binding specifically to a motif and wherein different types of antibody have different binding specificities.

14. (Previously presented) A method according to claim 3 wherein the number of different types of antibodies or fragments thereof provided on the array is suitable to capture at least 10% of the proteins, peptides, protein fragments or peptide fragments in the heterogeneous sample prior to fragmentation or, where the sample is a heterogeneous sample of protein fragments or peptide fragments, at least one fragment from at least 10% of the proteins or peptides in the unfragmented heterogeneous sample.
15. (Withdrawn) A method according to Claim 13 wherein the number of different types of binding molecule provided on the array is suitable to capture at least 50% of the proteins or peptides in the unfragmented sample or, where the sample is a heterogeneous sample of fragments of proteins or peptides, at least one fragment from at least 50% of the proteins or peptides in the unfragmented sample.
16. (Withdrawn) A method according to Claim 13 wherein the number of different types of binding molecule provided on the array is suitable to capture substantially 100% of the proteins or peptides in the unfragmented sample or, where the sample is a heterogeneous sample of fragments of proteins or peptides, at least one fragment from substantially 100% of the proteins or peptides in the unfragmented sample.
17. (Previously presented) A method according to claim 13 wherein the array has at least about 200, 250, 300, or more different types of antibodies or fragments thereof provided thereon.
18. Cancelled.
19. (Withdrawn) A method according to claim 13 wherein at least one of the types of the binding molecule is an aptamer.

20. (Withdrawn) A method according to claim 13 wherein at least one of the types of the binding molecule is a polynucleotide.
21. (Canceled)
22. (Canceled)
23. (Canceled)
24. (Previously presented) A method according to claim 1 wherein step (b) comprises characterizing the peptides, or protein or peptide fragments, in the heterogeneous classes by desorption mass spectrometry or collision induced dissociation mass spectrometry.
25. (Canceled)
26. (Previously presented) A method according to claim 3 wherein the information derived from step (b) is utilized in determining the abundance of the protein or peptide in the heterogeneous sample from which the protein fragment or peptide fragment derives.
27. (Previously presented) A method for identifying differences in composition between two or more heterogeneous fragmented or unfragmented samples of proteins, peptides, protein fragments or peptide fragments, comprising analyzing each sample by the method according to claim 1 and comparing the results, thereby to identify any differences.

Claims 28-49 (canceled).

50. (Previously presented) A method according to claim 1, wherein the array has at least 150 antibodies or fragments thereto fixed thereto.